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RAW SEQUENCE LISTING                    DATE: 04/26/2002
PATENT APPLICATION:  US/09/942,090      TIME: 14:24:43

Input Set : N:\Crf3\RULE60\09942090.raw
Output Set: N:\CRF3\04262002\I942090.raw
```

```
  1 <110> APPLICANT: Case, Casey C.
  2        Zhang, Lei
  3        Sangamo Biosciences, Inc.
  4 <120> TITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins
  5 <130> FILE REFERENCE: 019496-002000US
  6 <140> CURRENT APPLICATION NUMBER: 09/942,090
  7 <141> CURRENT FILING DATE: 2001-08-28
  9 <150> PRIOR APPLICATION NUMBER: 09/395,448
 10 <151> PRIOR FILING DATE: 1999-09-14
 12 <150> PRIOR APPLICATION NUMBER: 09/229,007
 13 <151> PRIOR FILING DATE: 1999-01-12
 14 <150> PRIOR APPLICATION NUMBER: 09/229,037
 15 <151> PRIOR FILING DATE: 1999-01-12
 16 <160> NUMBER OF SEQ ID NOS: 23
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 25
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Artificial Sequence
 23 <220> FEATURE:
 24 <223> OTHER INFORMATION: Description of Artificial Sequence:exemplary motif
 25        of C2H2 class of zinc finger proteins (ZFP)
W--> 26 <221> NAME/KEY: MOD_RES
 27 <222> LOCATION: (2)..(3)
 28 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 29 <221> MOD_RES
 30 <222> LOCATION: (4)..(5)
 31 <223> OTHER INFORMATION: Xaa = any amino acid, may be present or absent
W--> 32 <221> MOD_RES
 33 <222> LOCATION: (7)..(18)
 34 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 35 <221> MOD_RES
 36 <222> LOCATION: (20)..(22)
 37 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 38 <221> MOD_RES
 39 <222> LOCATION: (23)..(24)
 40 <223> OTHER INFORMATION: Xaa = any amino acid, may be present or absent
W--> 41 <400> 1
W--> 42        Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 43             1               5                   10                  15
W--> 44        Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His
 45                         20                  25
 47 <210> SEQ ID NO: 2
```

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Input Set : N:\Crf3\RULE60\09942090.raw
Output Set: N:\CRF3\04262002\I942090.raw

```
        48 <211> LENGTH: 10
        49 <212> TYPE: DNA
        50 <213> ORGANISM: Artificial Sequence
        51 <220> FEATURE:
        52 <223> OTHER INFORMATION: Description of Artificial Sequence:ZFP target site
        53       with two overlapping D-able subsites
W--> 54 <221> NAME/KEY: modified_base
        55 <222> LOCATION: (1)..(2)
        56 <223> OTHER INFORMATION: n = g, a, c or t
W--> 57 <221> modified_base
        58 <222> LOCATION: (5)
        59 <223> OTHER INFORMATION: n = g, a, c or t
W--> 60 <221> modified_base
        61 <222> LOCATION: (8)
        62 <223> OTHER INFORMATION: n = g, a, c or t
W--> 63 <221> modified_base
        64 <222> LOCATION: (9)
        65 <223> OTHER INFORMATION: n = a, c or t; if g, then position 10 cannot be g
        66       or t
W--> 67 <400> 2
W--> 68       nngkngknnn                                              10
        70 <210> SEQ ID NO: 3
        71 <211> LENGTH: 10
        72 <212> TYPE: DNA
        73 <213> ORGANISM: Artificial Sequence
        74 <220> FEATURE:
        75 <223> OTHER INFORMATION: Description of Artificial Sequence:ZFP target site
        76       with three overlapping D-able subsites
W--> 77 <221> NAME/KEY: modified_base
        78 <222> LOCATION: (1)..(2)
        79 <223> OTHER INFORMATION: n = g, a, c or t
W--> 80 <221> modified_base
        81 <222> LOCATION: (5)
        82 <223> OTHER INFORMATION: n = g, a, c or t
W--> 83 <221> modified_base
        84 <222> LOCATION: (8)
        85 <223> OTHER INFORMATION: n = g, a, c or t
W--> 86 <400> 3
W--> 87       nngkngkngk                                              10
        89 <210> SEQ ID NO: 4
        90 <211> LENGTH: 5
        91 <212> TYPE: PRT
        92 <213> ORGANISM: Artificial Sequence
        93 <220> FEATURE:
        94 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
        95 <400> SEQUENCE: 4
        96       Asp Gly Gly Gly Ser
        97         1               5
        99 <210> SEQ ID NO: 5
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100 <211> LENGTH: 5
101 <212> TYPE: PRT
102 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
105 <400> SEQUENCE: 5
106      Thr Gly Glu Lys Pro
107       1                 5
109 <210> SEQ ID NO: 6
110 <211> LENGTH: 9
111 <212> TYPE: PRT
112 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
115 <400> SEQUENCE: 6
116      Leu Arg Gln Lys Asp Gly Glu Arg Pro
117       1                 5
119 <210> SEQ ID NO: 7
120 <211> LENGTH: 4
121 <212> TYPE: PRT
122 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
125 <400> SEQUENCE: 7
126      Gly Gly Arg Arg
127       1
129 <210> SEQ ID NO: 8
130 <211> LENGTH: 5
131 <212> TYPE: PRT
132 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
135 <400> SEQUENCE: 8
136      Gly Gly Gly Gly Ser
137       1                 5
139 <210> SEQ ID NO: 9
140 <211> LENGTH: 8
141 <212> TYPE: PRT
142 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
145 <400> SEQUENCE: 9
146      Gly Gly Arg Arg Gly Gly Gly Ser
147       1                 5
149 <210> SEQ ID NO: 10
150 <211> LENGTH: 9
151 <212> TYPE: PRT
152 <213> ORGANISM: Artificial Sequence
153 <220> FEATURE:
```

RAW SEQUENCE LISTING   DATE: 04/26/2002
PATENT APPLICATION: US/09/942,090   TIME: 14:24:43

Input Set : N:\Crf3\RULE60\09942090.raw
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154 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
155 <400> SEQUENCE: 10
156   Leu Arg Gln Arg Asp Gly Glu Arg Pro
157   1   5
159 <210> SEQ ID NO: 11
160 <211> LENGTH: 12
161 <212> TYPE: PRT
162 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
165 <400> SEQUENCE: 11
166   Leu Arg Gln Lys Asp Gly Gly Gly Ser Glu Arg Pro
167   1   5   10
169 <210> SEQ ID NO: 12
170 <211> LENGTH: 16
171 <212> TYPE: PRT
172 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
175 <400> SEQUENCE: 12
176   Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Gly Ser Glu Arg Pro
177   1   5   10   15
179 <210> SEQ ID NO: 13
180 <211> LENGTH: 97
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence in
185   control construct
186 <400> SEQUENCE: 13
187   Val Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly Cys Gly
188   1   5   10   15
189   Lys Val Tyr Gly Gly His Asp Thr Val Val Gly His Leu Arg Trp His
190   20   25   30
191   Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg
192   35   40   45
193   Phe Thr Ala Ala Asp Glu Val Gly Leu His Lys Arg Thr His Thr Gly
194   50   55   60
195   Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met Leu Val
196   65   70   75   80
197   Val Ala Thr Gln Leu His Ile Lys Thr His Gln Asn Lys Lys Gly Gly
198   85   90   95
199   Ser
201 <210> SEQ ID NO: 14
202 <211> LENGTH: 292
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence
205 <220> FEATURE:
206 <223> OTHER INFORMATION: Description of Artificial Sequence:designed ZFP

```
     207           construct (from KpnI to BamHI) targeting 9-base
     208           pair target site in VEGF promoter
W--> 209  <221>  NAME/KEY: CDS
     210  <222>  LOCATION: (2)..(292)
W--> 211  <400>  14
     212           g gta ccg ggc aag aag aag cag cac atc tgc cac atc cag ggc tgt ggt 49
     213             Val Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly Cys Gly
     214             1               5                   10                  15
     215           aaa gtt tac ggc cgc tcc gac aac ctg acc cgc cac ctg cgc tgg cac  97
     216           Lys Val Tyr Gly Arg Ser Asp Asn Leu Thr Arg His Leu Arg Trp His
     217                       20                  25                  30
     218           acc ggc gag agg cct ttc atg tgt aca tgg tcc tac tgt ggt aaa cgc 145
     219           Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg
     220                       35                  40                  45
     221           ttc acc aac cgc gac acc ctg gcc cgc cac aag cgt acc cac acc ggt 193
     222           Phe Thr Asn Arg Asp Thr Leu Ala Arg His Lys Arg Thr His Thr Gly
     223                   50                  55                  60
     224           gag aag aaa ttt gct tgt ccg gaa tgt ccg aag cgc ttc atg cgc tcc 241
     225           Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met Arg Ser
     226             65                  70                  75                  80
     227           gac cac ctg tcc aag cac atc aag acc cac cag aac aag aag ggt gga 289
     228           Asp His Leu Ser Lys His Ile Lys Thr His Gln Asn Lys Lys Gly Gly
     229                       85                  90                  95
     230           tcc                                                             292
     231           Ser
     233  <210>  SEQ ID NO: 15
     234  <211>  LENGTH: 97
     235  <212>  TYPE: PRT
     236  <213>  ORGANISM: Artificial Sequence
     237  <220>  FEATURE:
     238  <223>  OTHER INFORMATION: Description of Artificial Sequence:designed ZFP
     239  <400>  SEQUENCE: 15
     240           Val Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly Cys Gly
     241             1               5                   10                  15
     242           Lys Val Tyr Gly Arg Ser Asp Asn Leu Thr Arg His Leu Arg Trp His
     243                       20                  25                  30
     244           Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg
     245                       35                  40                  45
     246           Phe Thr Asn Arg Asp Thr Leu Ala Arg His Lys Arg Thr His Thr Gly
     247                   50                  55                  60
     248           Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met Arg Ser
     249             65                  70                  75                  80
     250           Asp His Leu Ser Lys His Ile Lys Thr His Gln Asn Lys Lys Gly Gly
     251                       85                  90                  95
     252           Ser
     254  <210>  SEQ ID NO: 16
     255  <211>  LENGTH: 25
     256  <212>  TYPE: DNA
     257  <213>  ORGANISM: Artificial Sequence
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/26/2002
PATENT APPLICATION: US/09/942,090   TIME: 14:24:44

    Input Set : N:\Crf3\RULE60\09942090.raw
    Output Set: N:\CRF3\04262002\I942090.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,3,4,5,7,8,9,10,11,12,13,14,15,16,17,18,20,21,22,23,24
Seq#:2; N Pos. 1,2,5,8,9,10
Seq#:3; N Pos. 1,2,5,8

VERIFICATION SUMMARY   DATE: 04/26/2002
PATENT APPLICATION: **US/09/942,090**   TIME: 14:24:44

Input Set : **N:\Crf3\RULE60\09942090.raw**
Output Set: **N:\CRF3\04262002\I942090.raw**

```
L:26  M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:29  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:32  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:35  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:38  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:41  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:42  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:44  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16
L:54  M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:57  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:60  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:63  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:67  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:68  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:77  M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:80  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:83  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:86  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:87  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:209 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:211 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14
```